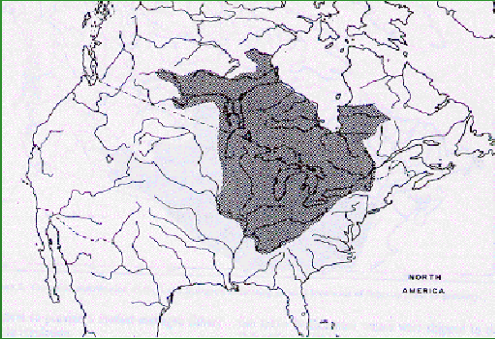# Linking Lake Sturgeon Demographics and Genetics

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Background and issues facing management directed at lake sturgeon recovery

I. Where were populations historically and what is the current distribution and abundance?

II. What were the causes for declines and extirpation? Have impediments to restoration been overcome?


VS

III. What are the limiting factors affecting lake sturgeon recovery and what are the most viable management options

Rehabilitation Strategies

- Genetic markers provide a novel method for examining many demographic and life history characteristics of lake sturgeon in the Great Lakes

- By combining demographic and population genetic principles in a modeling framework we can predict what critical factors contribute to probability of long-term persistence and offer recommendations for or against alterative management options

- We can help select populations in greatest need of management

Likelihood of population persistence due to demographic, genetic, and environmental factors
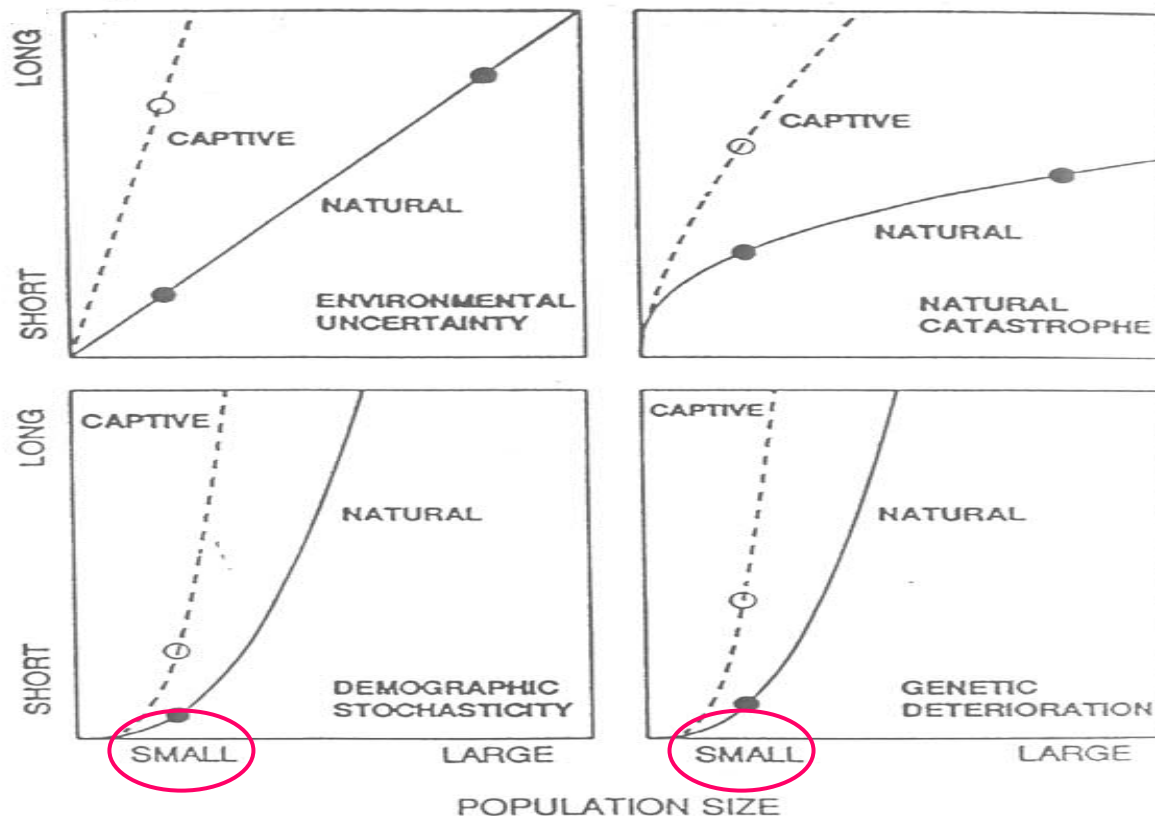
after Schaffer (1987) and Lande 1991

Are current estimates of population abundance correlated with estimates of genetic diversity?
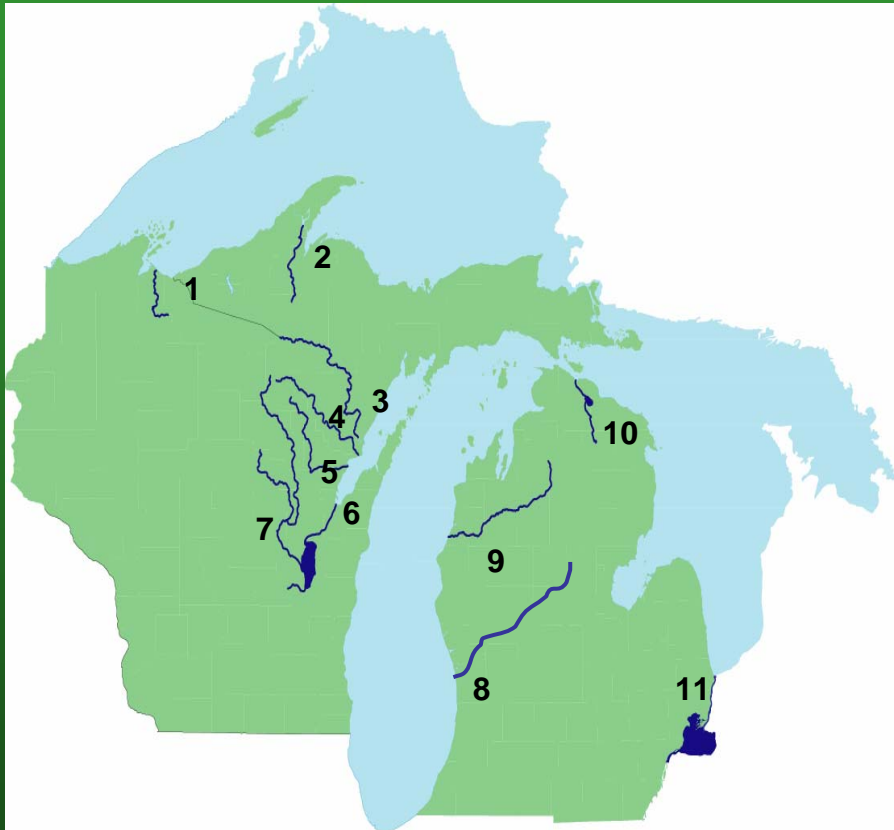
Pop. No	Run Size*	No. Allele	Het.	No. hapl.	Hapl. Div
1	350	2.9	0.65	5	0.73
2	200	3.1	0.61	4	0.60
3	200	2.9	0.59	9	0.83
4	200	3.0	0.64	9	0.91
5	Small	2.9	0.61	5	0.68
6	Small	3.1	0.60	5	0.75
7	22,000	3.1	0.62	8	0.83
8	Small	3.4	0.65	3	0.47
9	Small	3.0	0.58	5	0.68
10	120	3.4	0.68	7	0.77
11	small	3.3	0.69	7	0.75

* From Holey et al. (2000)

Data from DeHaan et al. (in prep) 8 microsatellite loci and mtDNA sequence data

Objectives

- Determine how demographic stochasticity varies as a function of initial population size (i.e., affecting population extinction probability)

- Determine how inbreeding accumulates as a function of initial population size

- Future – how do feedbacks between inbreeding and demographics affect the linked population/genetic system

Modeling Approach and Structure

- Individual-based model

- Tracks parentage, allele frequency, demographic variables

Empirical Applications

- Make predictions about fate of remnant Great Lakes populations of Lake Sturgeon
- Make predictions of plausible contributions of inbreeding to probability of population persistence and influences of stocking strategies

Model Structure

Initialize population
  -Number of individuals
  -Age and sex of individuals
  -Genotype (including unique id)

Select individuals for breeding each year
Generate random number of spawning bouts for ids selected
Perform 1:1 mating for each spawning bout

Generate random number of offspring for each mating
Assign age, sex, genotype for each offspring

Randomly "kill" individuals based on stage-specific mortality rates
Update ages
Calculate inbreeding coefficient for all new individuals
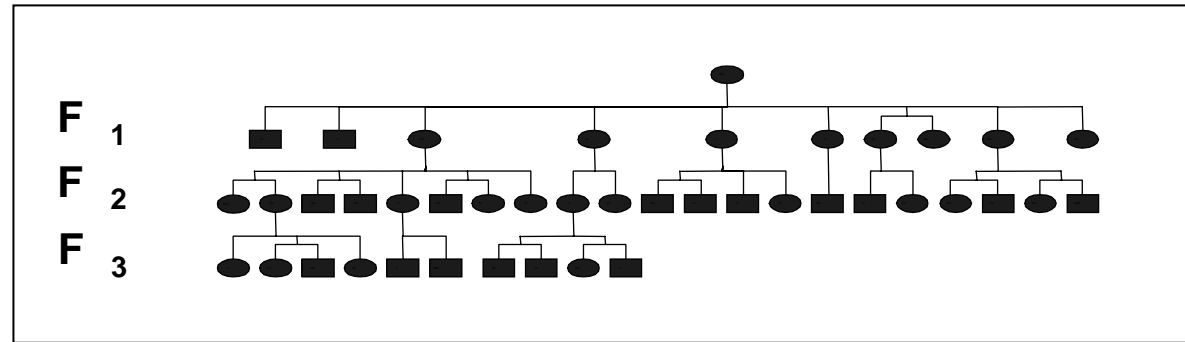
At end of simulation, calculate
  -Total surviving population
  -Mean inbreeding for each year for each repetition
  -Number of unique id genes retained

Model Parameters

Male age at first breeding	15 years
Adult male probability of spawning	0.50 (spawn roughly every other year)
Female age at first breeding	20 years
Adult female probability of spawning	0.33 (spawn roughly every three years)
Juvenile Mortality	30% per year
Adult Mortality	5% per year
Number of batches per spawning season per adult (mating random)	Negative exponential with mean=2.5 and std=1.9
Number of young produced per batch	Negative exponential with mean=0.55 and std=0.9
*Note: this combination of parameter values results in average population growth rates near 0	

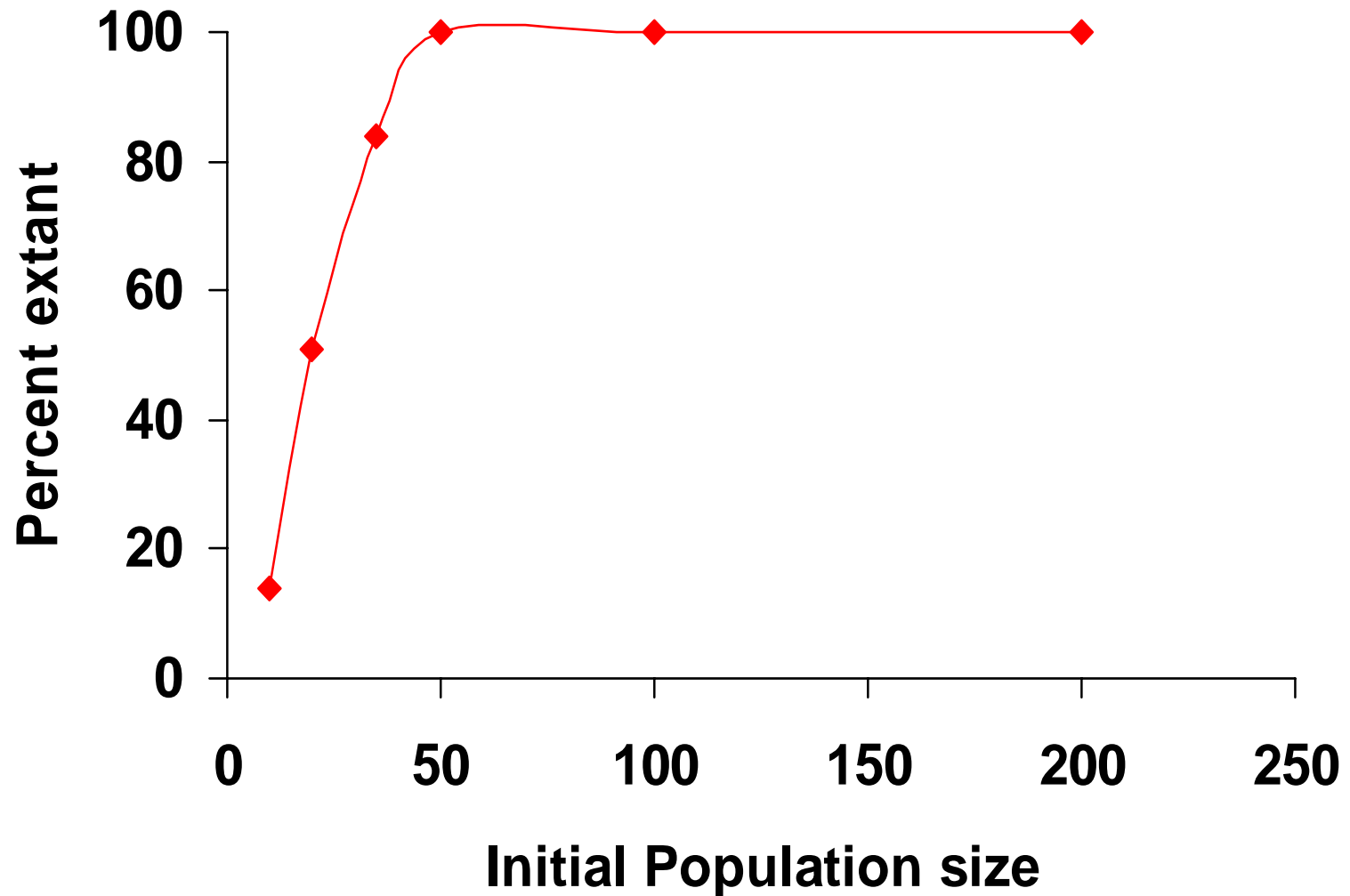# Example of multi-generational pedigree and effects of mating system on relatedness and inbreeding

	Male 1				Male 2			
ID	F1	O1	O2	O3	O4	F2	O5	O6	O7	O8
O1			Θ	Θ	Θ		0	0	0	0
O2				Θ	Θ		0	0	0	0
O3					Θ		0	0	0	0
O4							0	0	0	0
O5								Θ	Θ	Θ
O6									Θ	Θ
O7										Θ
O8										

57% offspring unrelated
$\Theta = 0.107$

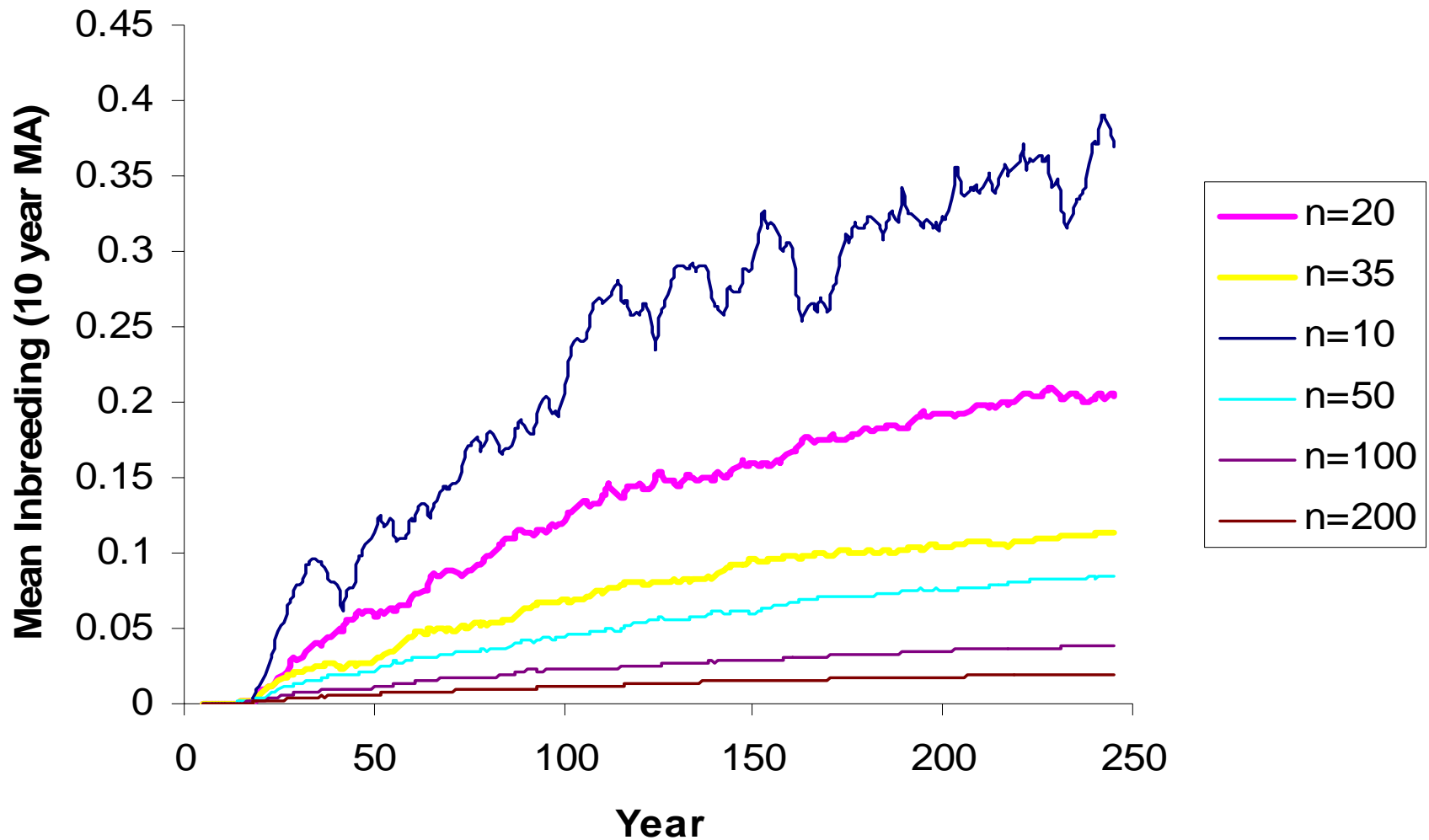|	Male 1		Male2		Male 1		Male 2	
ID	F1	O1	O2	O3	O4	F2	O5	O6	O7	O8
O1			Θ	$\Theta/2$	$\Theta/$		$\Theta/2$	$\Theta/2$	0	0
O2				$\Theta/2$	$\Theta/2$		$\Theta/2$	$\Theta/2$	0	0
O3					Θ		0	0	$\Theta/2$	$\Theta/2$
O4							0	0	$\Theta/2$	$\Theta/2$
O5								Θ	$\Theta/2$	$\Theta/2$
O6									$\Theta/2$	$\Theta/2$
O7										Θ
O8										

28% offspring unrelated
$\Theta = 0.107$

Results: probability of extinction over 250 yrs as a function of initial population size

Results: estimates of expected loss of alleles

Legend:
- n=20
- n=35
- n=50
- n=100
- n=10

Y-axis: **Proportion of genes retained**

X-axis: **Rate of Population Increase (N250/N0)**
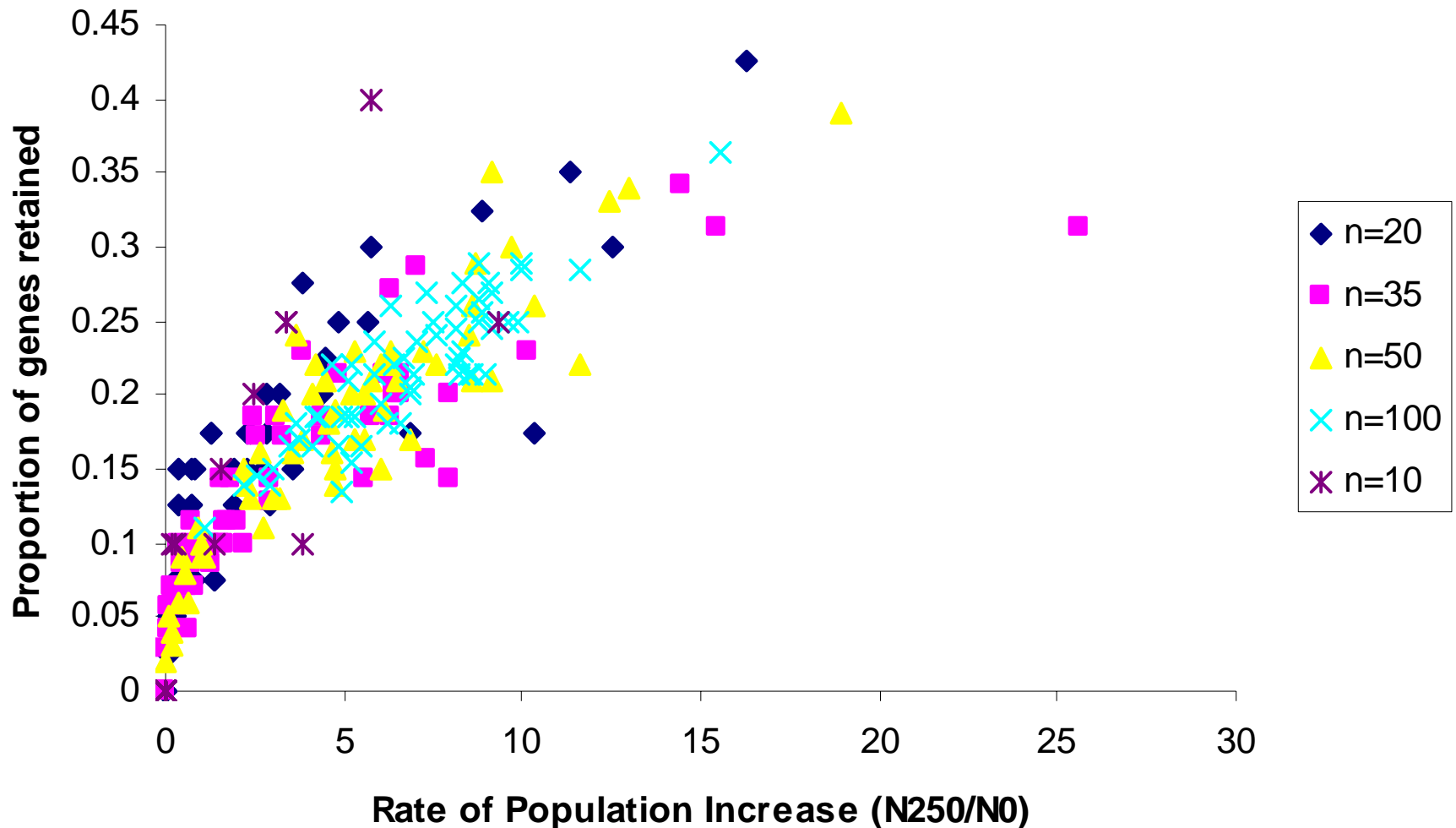
Results: estimates of expected inbreeding in populations of different initial size

Conclusions

- Initial populations less than 50 have a high likelihood of extinction within 250 years due to demographic stochasticity

- The proportion of genes retained depends primarily on the overall rate of population growth, independent of initial population size

- Accumulation of inbreeding strongly depends on initial population size. Populations of 50 or less accumulate high degrees of inbreeding within 250 years

Future Directions

- Analyses of genetic effects incorporated into overall assessments of interacting genetic, demographic, and environmental risks faced by small populations

- Include density-dependence and/or habitat dependency in models

- Evaluate different supplementation strategies that address both genetic and demographic concerns

- Identify populations where supplementation is necessary and where it is most likely to be beneficial

Log fitness (or fecundity/viability)

A

Inbreeding depression

Slope = -B
'Inbreeding load'

$\ln(S) = \ln(S_0) - BF = A - BF$

Inbreeding Coefficient (F)

0.25   0.5   0.75   1.0
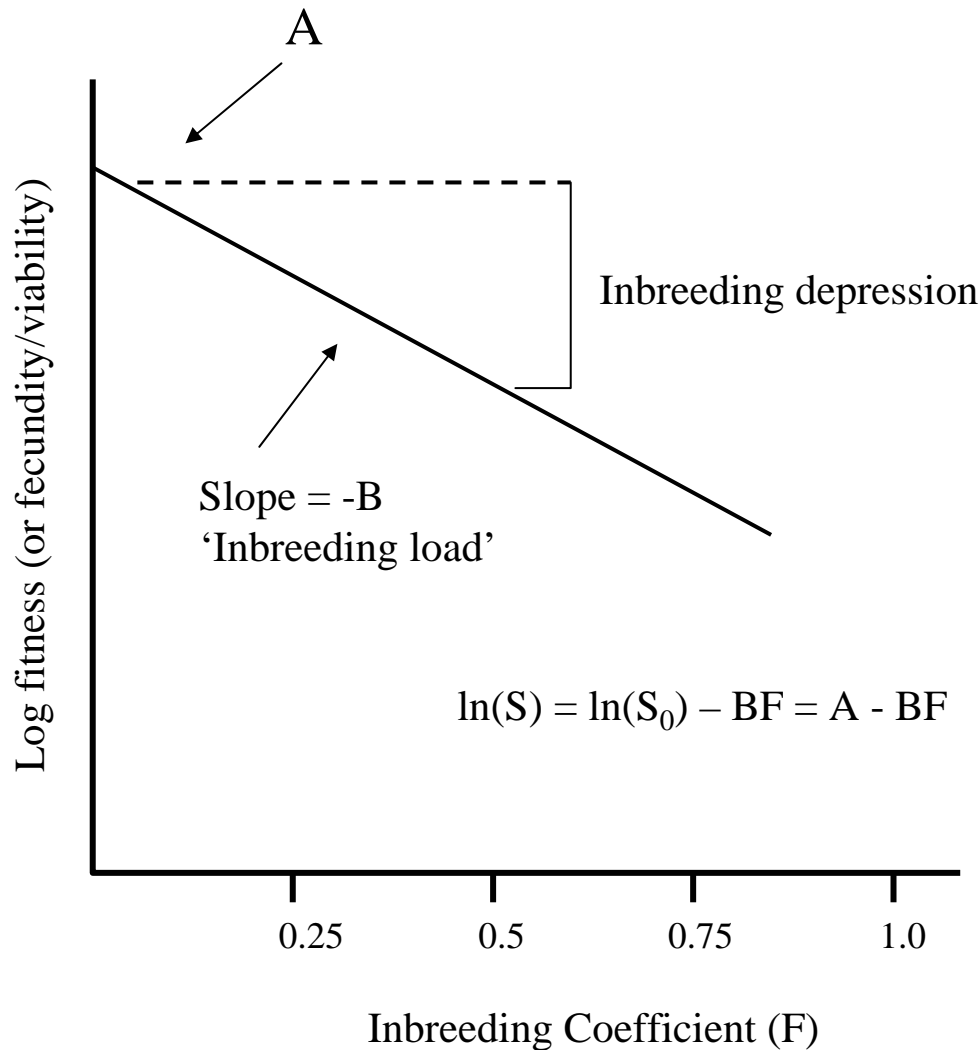
Morton et al. (1956) $S = S_0 e^{-BF}$
Where S is the probability of
an individual with level inbreeding
F surviving to a specified age, S_0 is
the viability of non-inbred individuals,
and B is a measure of how fast viability
declines with inbreeding. A is $\ln(S_0)$ and
measures the effect of environmental
sources of mortality plus mortality due to
homozygosity not associated with F.

Extinction Vortex

Small Size

**Reduced
Growth Rate**

**Increased
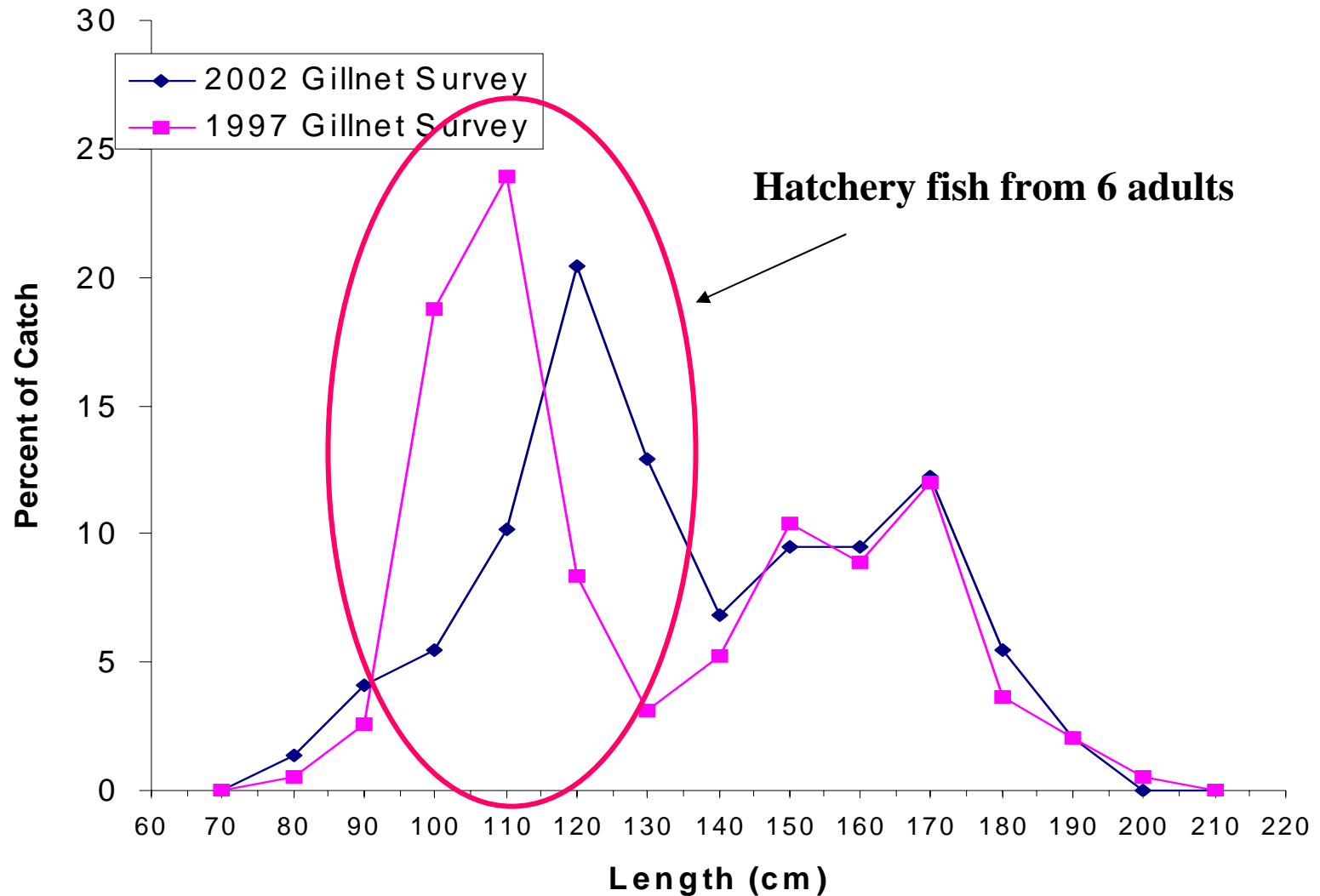inbreeding**

**Decreased
Reproduction
& survival**
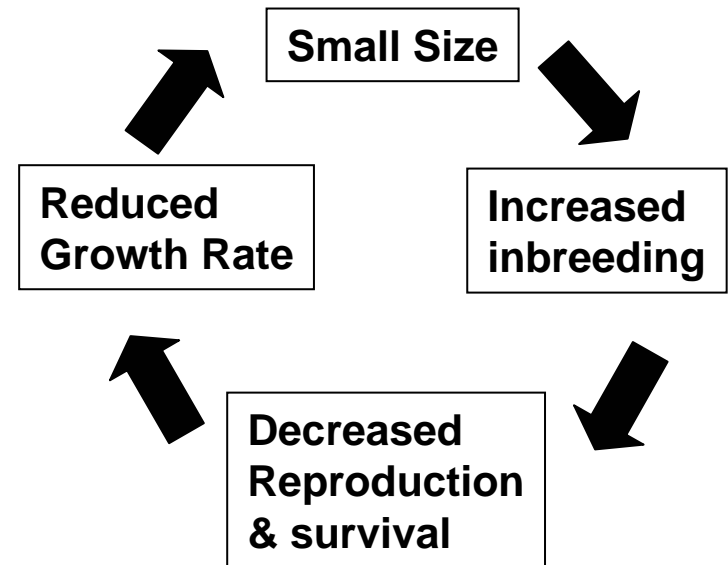
How relevant are projections of population levels of inbreeding for extant Great Lakes populations?
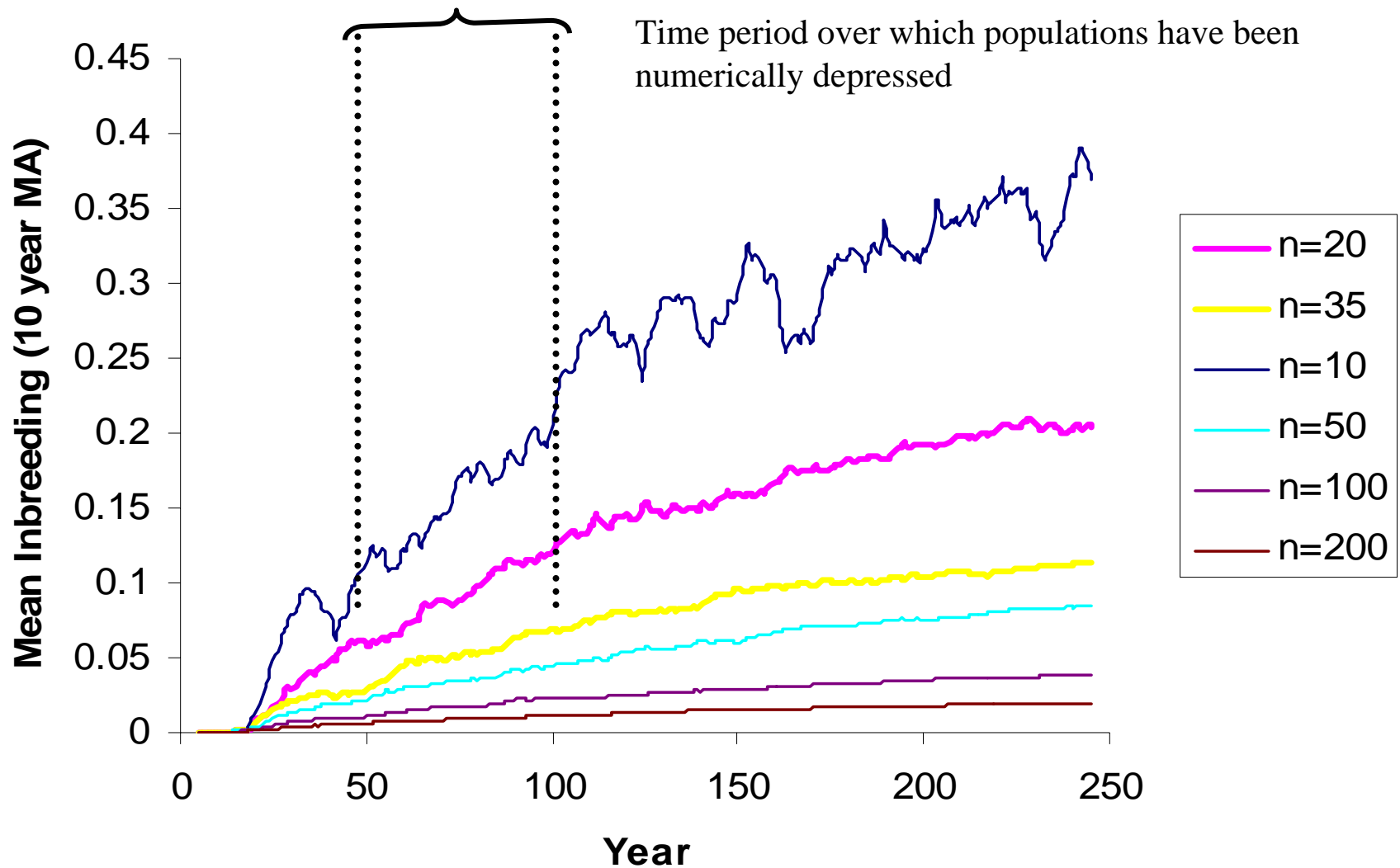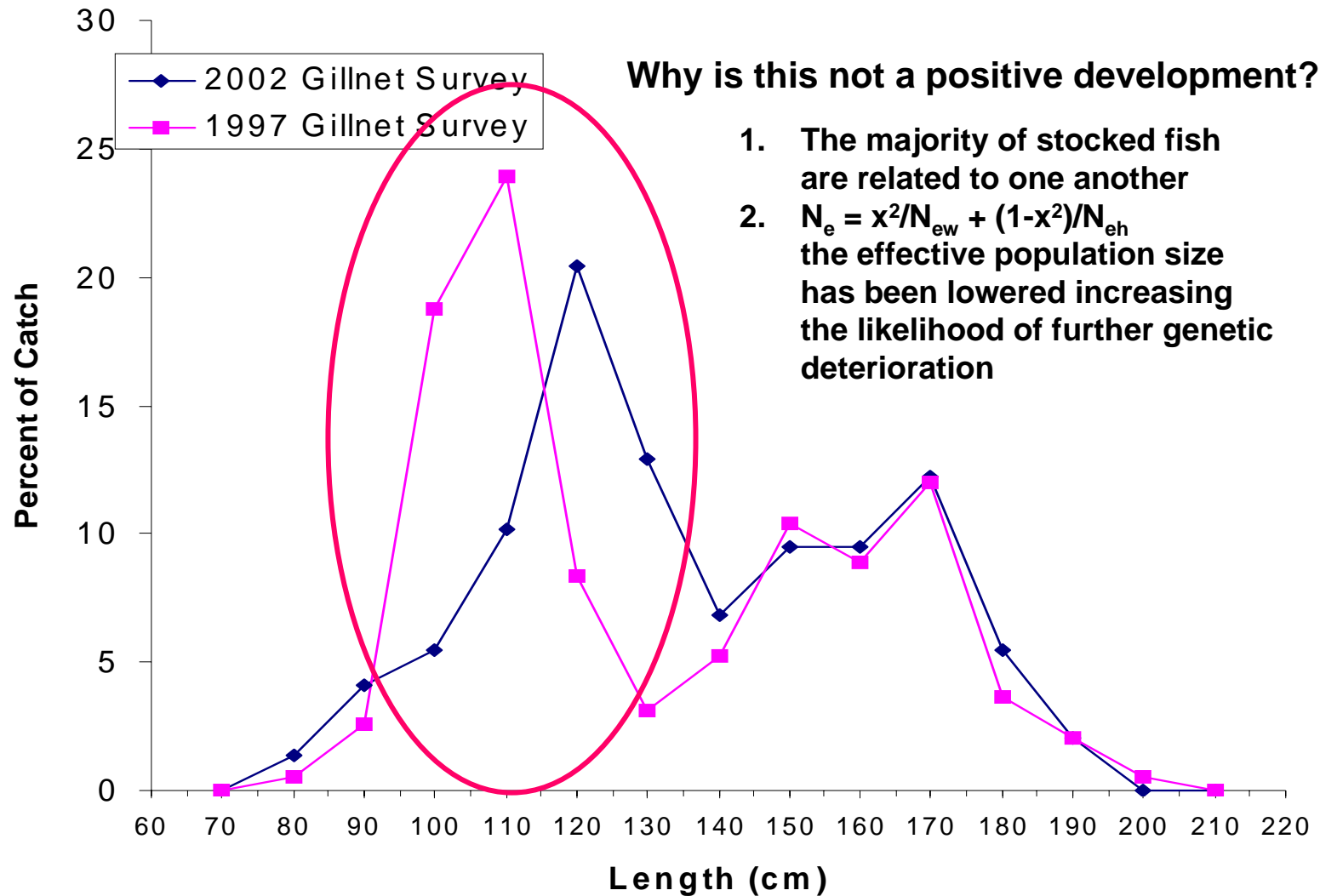
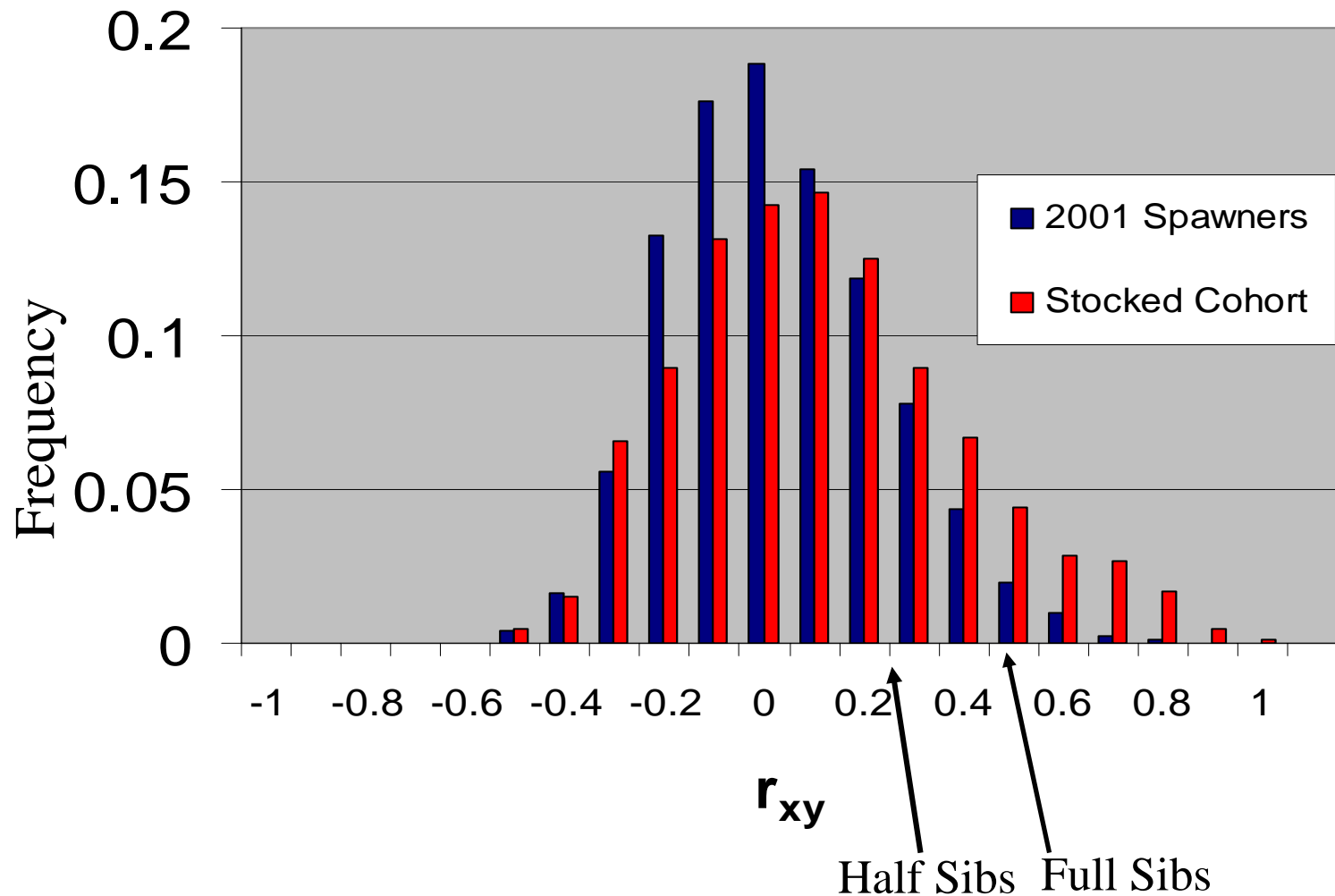# Size distribution for Black Lake Sturgeon sampled during 2 time periods
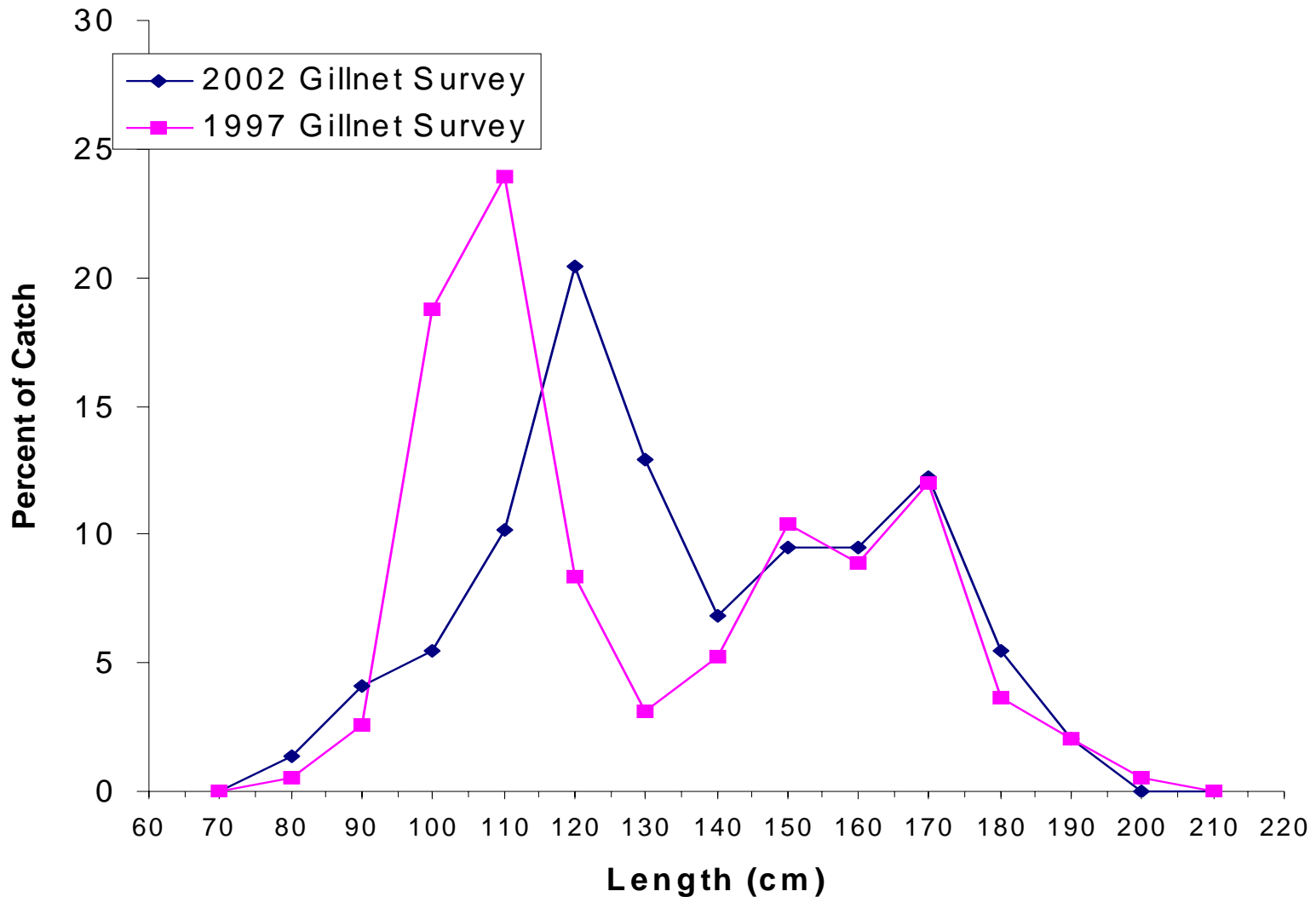
Size distribution for Black Lake Sturgeon sampled during 2 time periods

Size distribution for Black Lake Sturgeon sampled during 2 time periods

Why is this not a positive development?

1. **The majority of stocked fish are related to one another**
2. $N_e = x^2/N_{ew} + (1-x^2)/N_{eh}$
   the effective population size has been lowered increasing the likelihood of further genetic deterioration

Molecular markers establish levels of inter-individual relatedness (r_{xy}) as a surrogate measure of kinship relationship (θ)

Acknowledgements